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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Israeli, Ron S.
Heston, Warren D.W.
Fair, William R.

(ii) TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN

(iii) NUMBER OF SEQUENCES: 38

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham
(B) STREET: 30 Rockefeller Plaza
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States of America
(F) ZIP: 10112

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 1747/41426

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2653 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(F) TISSUE TYPE: Carcinoma

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(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate-Specific Membrane Antigen

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 262..2511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCAAAAGGG GCCGGATTC CTTCTCCTGG AGGCAGATGT TGCCTCTCTC TCTCGCTCGG	60
ATGGGTCAG TGCACCTCTAG AAACACTGCT GTGGTGGAGA AACTGGACCC CAGGTCTGGA	120
GCGAATTCCA GCCTGCAGGG CTGATAAGCG AGGCATTAGT GAGATTGAGA GAGACTTAC	180
CCCGCCGTGG TGGTGGAGG GCGCGCAGTA GAGCAGCAGC ACAGGCGCGG GTCCCGGGAG	240
GCCGGCTCTG CTCGCGCCGA G ATG TGG AAT CTC CTT CAC GAA ACC GAC TCG Met Trp Asn Leu Leu His Glu Thr Asp Ser	291
1 5 10	
GCT GTG GCC ACC GCG CGC CGC CCG CGC TGG CTG TGC GCT GGG GCG CTG Ala Val Ala Thr Ala Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu	339
15 20 25	
GTG CTG GCG GGT GGC TTC TTT CTC CTC GGC TTC CTC TTC GGG TGG TTT Val Leu Ala Gly Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe	387
30 35 40	
ATA AAA TCC TCC AAT GAA GCT ACT AAC ATT ACT CCA AAG CAT AAT ATG Ile Lys Ser Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met	435
45 50 55	
AAA GCA TTT TTG GAT GAA TTG AAA GCT GAG AAC ATC AAG AAG TTC TTA Lys Ala Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu	483
60 65 70	
TAT AAT TTT ACA CAG ATA CCA CAT TTA GCA GGA ACA GAA CAA AAC TTT Tyr Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe	531
75 80 85 90	
CAG CTT GCA AAG CAA ATT CAA TCC CAG TGG AAA GAA TTT GGC CTG GAT Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp	579
95 100 105	
TCT GTT GAG CTA GCA CAT TAT GAT GTC CTG TTG TCC TAC CCA AAT AAG Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys	627
110 115 120	
ACT CAT CCC AAC TAC ATC TCA ATA ATT AAT GAA GAT GGA AAT GAG ATT Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile	675
125 130 135	
TTC AAC ACA TCA TTA TTT GAA CCA CCT CCT CCA GGA TAT GAA AAT GTT Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val	723
140 145 150	
TCG GAT ATT GTA CCA CCT TTC AGT GCT TTC TCT CCT CAA GGA ATG CCA Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser Pro Gln Gly Met Pro	771
155 160 165 170	

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GAG GGC GAT CTA GTG TAT GTT AAC TAT GCA CGA ACT GAA GAC TTC TTT Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe 175 180 185	819
AAA TTG GAA CGG GAC ATG AAA ATC AAT TGC TCT GGG AAA ATT GTA ATT Lys Leu Glu Arg Asp Met Lys Ile Asn Cys Ser Gly Lys Ile Val Ile 190 195 200	867
GCC AGA TAT GGG AAA GTT TTC AGA GGA AAT AAG GTT AAA AAT GCC CAG Ala Arg Tyr Gly Lys Val Phe Arg Gly Asn Lys Val Lys Asn Ala Gln 205 210 215	915
CTG GCA GGG GCC AAA GGA GTC ATT CTC TAC TCC GAC CCT GCT GAC TAC Leu Ala Gly Ala Lys Gly Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr 220 225 230	963
TTT GCT CCT GGG GTG AAG TCC TAT CCA GAT GGT TGG AAT CTT CCT GGA Phe Ala Pro Gly Val Lys Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly 235 240 245 250	1011
GGT GGT GTC CAG CGT GGA AAT ATC CTA AAT CTG AAT GGT GCA GGA GAC Gly Gly Val Gln Arg Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp 255 260 265	1059
CCT CTC ACA CCA GGT TAC CCA GCA AAT GAA TAT GCT TAT AGG CGT GGA Pro Leu Thr Pro Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly 270 275 280	1107
ATT GCA GAG GCT GTT GGT CTT CCA AGT ATT CCT GTT CAT CCA ATT GGA Ile Ala Glu Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly 285 290 295	1155
TAC TAT GAT GCA CAG AAG CTC CTA GAA AAA ATG GGT GGC TCA GCA CCA Tyr Tyr Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro 300 305 310	1203
CCA GAT AGC AGC TGG AGA GGA AGT CTC AAA GTG CCC TAC AAT GTT GGA Pro Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly 315 320 325 330	1251
CCT GGC TTT ACT GGA AAC TTT TCT ACA CAA AAA GTC AAG ATG CAC ATC Pro Gly Phe Thr Gly Asn Phe Ser Thr Gln Lys Val Lys Met His Ile 335 340 345	1299
CAC TCT ACC AAT GAA GTG ACA AGA ATT TAC AAT GTG ATA GGT ACT CTC His Ser Thr Asn Glu Val Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu 350 355 360	1347
AGA GGA GCA GTG GAA CCA GAC AGA TAT GTC ATT CTG GGA GGT CAC CGG Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg 365 370 375	1395
GAC TCA TGG GTG TTT GGT ATT GAC CCT CAG AGT GGA GCA GCT GTT Asp Ser Trp Val Phe Gly Gly Ile Asp Pro Gln Ser Gly Ala Ala Val 380 385 390	1443
GTG CAT GAA ATT GTG AGG AGC TTT GGA ACA CTG AAA AAG GAA GGG TGG Val His Glu Ile Val Arg Ser Phe Gly Thr Leu Lys Glu Gly Trp 395 400 405 410	1491
AGA CCT AGA AGA ACA ATT TTG TTT GCA AGC TGG GAT GCA GAA GAA TTT Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe	1539

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415	420	425	
GGT CTT CTT GGT TCT ACT GAG TGG GCA GAG GAG AAT TCA AGA CTC CTT Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu 430	435	440	1587
CAA GAG CGT GGC GTG GCT TAT ATT AAT GCT GAC TCA TCT ATA GAA GGA Gln Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly 445	450	455	1635
AAC TAC ACT CTG AGA GTT GAT TGT ACA CCG CTG ATG TAC AGC TTG GTA Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu Val 460	465	470	1683
CAC AAC CTA ACA AAA GAG CTG AAA AGC CCT GAT GAA GGC TTT GAA GGC His Asn Leu Thr Lys Glu Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly 475	480	485	1731
AAA TCT CTT TAT GAA AGT TGG ACT AAA AAA AGT CCT TCC CCA GAG TTC Lys Ser Leu Tyr Glu Ser Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe 495	500	505	1779
AGT GGC ATG CCC AGG ATA AGC AAA TTG GGA TCT GGA AAT GAT TTT GAG Ser Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu 510	515	520	1827
GTG TTC TTC CAA CGA CTT GGA ATT GCT TCA GGC AGA GCA CGG TAT ACT Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr 525	530	535	1875
AAA AAT TGG GAA ACA AAC AAA TTC AGC GGC TAT CCA CTG TAT CAC AGT Lys Asn Trp Glu Thr Asn Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser 540	545	550	1923
GTC TAT GAA ACA TAT GAG TTG GTG GAA AAG TTT TAT GAT CCA ATG TTT Val Tyr Glu Thr Tyr Glu Leu Val Glu Lys Phe Tyr Asp Pro Met Phe 555	560	565	1971
AAA TAT CAC CTC ACT GTG GCC CAG GTT CGA GGA GGG ATG GTG TTT GAG Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Gly Met Val Phe Glu 575	580	585	2019
CTA GCC AAT TCC ATA GTG CTC CCT TTT GAT TGT CGA GAT TAT GCT GTA Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val 590	595	600	2067
GTT TTA AGA AAG TAT GCT GAC AAA ATC TAC AGT ATT TCT ATG AAA CAT Val Leu Arg Lys Tyr Ala Asp Lys Ile Tyr Ser Ile Ser Met Lys His 605	610	615	2115
CCA CAG GAA ATG AAG ACA TAC AGT GTA TCA TTT GAT TCA CTT TTT TCT Pro Gln Glu Met Lys Thr Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser 620	625	630	2163
GCA GTA AAG AAT TTT ACA GAA ATT GCT TCC AAG TTC AGT GAG AGA CTC Ala Val Lys Asn Phe Thr Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu 635	640	645	2211
CAG GAC TTT GAC AAA AGC AAC CCA ATA GTA TTA AGA ATG ATG AAT GAT Gln Asp Phe Asp Lys Ser Asn Pro Ile Val Leu Arg Met Met Asn Asp 655	660	665	2259

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CAA CTC ATG TTT CTG GAA AGA GCA TTT ATT GAT CCA TTA GGG TTA CCA Gln Leu Met Phe Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro 670 675 680	2307
GAC AGG CCT TTT TAT AGG CAT GTC ATC TAT GCT CCA AGC AGC CAC AAC Asp Arg Pro Phe Tyr Arg His Val Ile Tyr Ala Pro Ser Ser His Asn 685 690 695	2355
AAG TAT GCA GGG GAG TCA TTC CCA GGA ATT TAT GAT GCT CTG TTT GAT Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp 700 705 710	2403
ATT GAA AGC AAA GTG GAC CCT TCC AAG GCC TGG GGA GAA GTG AAG AGA Ile Glu Ser Lys Val Asp Pro Ser Lys Ala Trp Gly Glu Val Lys Arg 715 720 725 730	2451
CAG ATT TAT GTT GCA GCC TTC ACA GTG CAG GCA GCT GCA GAG ACT TTG Gln Ile Tyr Val Ala Ala Phe Thr Val Gln Ala Ala Ala Glu Thr Leu 735 740 745	2499
AGT GAA GTA GCC TAAGAGGATT CTTTAGAGAA TCCGTATTGA ATTTGTGTGG Ser Glu Val Ala 750	2551
TATGTCACTC AGAAAAGAATC GTAATGGGTA TATTGATAAA TTTTAAAATT GGTATATTG AAATAAAGTT GAATATTATA TATAAAAAAA AAAAAAAA AA	2611
	2653

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 750 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg 1 5 10 15
Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe 20 25 30
Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu 35 40 45
Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu 50 55 60
Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile 65 70 75 80
Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile 85 90 95
Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His 100 105 110
Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile

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115	120	125	
Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe			
130	135	140	
Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro			
145	150	155	160
Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr			
165	170	175	
Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met			
180	185	190	
Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val			
195	200	205	
Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly			
210	215	220	
Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys			
225	230	235	240
Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Val Gln Arg Gly			
245	250	255	
Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr			
260	265	270	
Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly			
275	280	285	
Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys			
290	295	300	
Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg			
305	310	315	320
Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn			
325	330	335	
Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val			
340	345	350	
Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro			
355	360	365	
Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly			
370	375	380	
Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg			
385	390	395	400
Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile			
405	410	415	
Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr			
420	425	430	
Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala			
435	440	445	

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Tyr	Ile	Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val
450															460
Asp	Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu
465															480
Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu	Ser
															495
485															
Trp	Thr	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	Arg	Ile	
															510
Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	Gln	Arg	Leu
															525
Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	Trp	Glu	Thr	Asn
															540
Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val	Tyr	Glu	Thr	Tyr	Glu
545															560
Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe	Lys	Tyr	His	Leu	Thr	Val
															575
Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser	Ile	Val
															590
Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr	Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala
															605
Asp	Lys	Ile	Tyr	Ser	Ile	Ser	Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr
															620
Tyr	Ser	Val	Ser	Phe	Asp	Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr
625															640
Glu	Ile	Ala	Ser	Lys	Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser
															655
Asn	Pro	Ile	Val	Leu	Arg	Met	Met	Asn	Asp	Gln	Leu	Met	Phe	Leu	Glu
															670
Arg	Ala	Phe	Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg
															685
His	Val	Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser
															700
Phe	Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
705															720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala	Ala
															735
Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala		
740															

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid

(D)

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- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Leu Tyr Glu Ser Xaa Thr Lys
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Tyr Pro Asp Gly Xaa Asn Leu Pro Gly Gly Gly Val Gln Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Phe Tyr Asp Pro Met Phe Lys
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ile Tyr Asn Val Ile Gly Thr Leu Lys
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Specific Membrane Antigen

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Phe Leu Tyr Xaa Xaa Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln
1 5 10 15
Asn Phe Gln Leu Ala Lys
20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Asp Val
1 5 10 15
Lys

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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Pro Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val
1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile
1 5 10 15

Glu Ser Lys

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Xaa Xaa Glu
1 5 10 15

Ser Thr Glu Glu Ala Glu
20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTYTAYGAYC CNATGTT

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

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- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AACATNGGRT CRTARAA

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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATHTAYAAYG TNATHGG

17

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien

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(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCDATNACRT TRTADAT

17

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCNGCNGAYT AYTTCGC

17

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCRAARTART CNGCNGG

17

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(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACNGARCARA AYTTYCARCT

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGYTGRAART TYTGYTCNGT

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GARCARAAYT TYCARCT

17

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGYTGRAART TYTGYTC

17

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGGGAYGCNG ARGARTTYGG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCRAAYTCYT CNGCRTCCCA

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGGGAYGCNG ARGARTT

17

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapien
 (F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAYTCYTCNG CRTCCCA

17

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 780 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TACACTTATC CCATTGGAC ATGCCACCT TGGAACTGGA GACCCTTACA CCCCAGGCTT	60
CCCTTCGTTTC AACCACACCC ANNNNGTTCC ACCAGTTGAA TCTTCAGGAC TACCCCACAT	120
TGCTGTTCACT ACCATCTCTA GCAGTGCAGC AGCCAGGCTG TTCAGCAAAA TGGATGGAGA	180
CACATGCTCT GANAGNNNGTT GGAAAGGTGC GATCCANNNT TCCGTAAAGG TNNGACNNAA	240
CAAAGCAGGA GANNNNGCCA GANTAAATGGT GAAACTAGAT GTGAACAATT CCATGAAAGA	300
CAGGAAGATT CTGAACATCT TCGGTGCTAT CCAGGGATTG GAAGAACCTG ATCGGTATGT	360
TGTGATTGGA GCCCAGAGAG ACTCCTGGGG CCCAGGAGTG GCTAAAGCTG GCACTGGAAC	420
TGCTATATTG TTGGAACCTTG CCCGTGTGAT CTCAGACATA GTGAAAAACG AGGGCTACAA	480
ACCGAGGCAGA AGCATCATCT TTGCTAGCTG GAGTGCAGGA GACTACGGAG CTGTGGGTGC	540
TACTGAATGG CTGGAGGGGT ACTCTGCCAT GCTGCATGCC AAAGCTTCA CTTACATCAN	600
NGCTTGGATG CTCCAGTCCT GGGAGCAAGC CATGTCAAGA TTTCTGCCAG CCCCTTGCTG	660
TATATGCTGC TGGGGAGTAT TATGAAGGGG GTGAAGAAC CAGCAGCAGT CTCAGAGAGC	720

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NNNNCTCTAT AACAGACTTG GCCCAGACTG GGTAAAAGCA GTTGTTCCTC TTGGCCTGGA 780

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 660 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TGCAGAAAAG CTATTCAAAA ACATGGAAGG AAACTGTCT CCTAGTTGGA ATATAGATT	60
CTCATGTAAG CTGGAACCTTT CACAGAAATCA AAATGTGAAG CTCACTGTGA ACAATGTACT	120
GAAAGAAAACA AGAATACTTA ACATCTTGG CGTTATTAAA GGCTATGAGG AACCAGACCG	180
CTACATTGTA GTAGGAGGCC AGAGAGACGC TTGGGGCCCT GGTNGTTGCG AAGTCCAGTG	240
TGGGAACAGG TCTTNCTGTT GAAACTTGCC CAAGTATTCT CAGATATGAT TTCAAAAGAT	300
GGATTTAGAC CCAGCAGGAG TATTATCTT GCCAGCTGGA CTGCAGGAGA CTATGGAGCT	360
GTTGGTCCGA CTGAGTGGCT GGAGGGGTAC CTTTCATCTT TGCATCTAAA GNNNGCTTTC	420
ACTTACATTA ATNCTGGATA AAGTCGTCTT GGGTACTAGC AACTTCAAGG TTTCTGCCAG	480
CCCCCTATTA TATACACTTA TGGGGAAGAT AATGCAGGAN NCGTAAAGCA TCCGANNNNN	540
NNNTTGATGG AAAATATCTA TATCGAAACA GTAATTGGAT TAGCAAATT GAGGAACCTT	600
CCTTGGACAA TGCTGCATTC CCTTTCTTG CATATTCAAGG AATCCCAGCA GTTTCTTCT	660

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

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TATGGAAAGGA GACTGTCCCT CTGACTGGAA AACAGACTCT ACATGTAGGA TGGTAACCTC	60
AGAAAGCAAG AATGTGAAGC TCACTGTGAG CAATGTGCTG AAAGAGATAA AAATTCTTAA	120
CATCTTGGA GTTATTAAAG GCTTTGTAGA ACCAGATCAC TATGTTGTAG TTGGGGCCCA	180
GAGAGATGCA TGGGGCCCTG GAGCTGCAAA ATCNCGGTGT AGGCACAGCT CTCCTATTGA	240
AACTTGCCTA GATGTTCTCA GATATGGTCT TAAAAGATGG GTTTCAGCCC AGCAGAAAGCA	300
TTATCTTGCG CAGTTGGAGT GCTGGAGACT TTGGATCGGT TGGTGCCACT GAATGGCTAG	360
AGGGATACCT TTCGTCNCCT GCATTTAAAG GCTTTCACTT ATATTAATCT GGATAAAAGCG	420
GTTCTTGGTA CCAGCAACTT CAAGGTTTCTT GCCAGCCCAC TGTGTATAC GCTTATTGAG	480
AAAACAATGC AAAATGTGAA GCATCCGGTT ACTGGGCAAT TTCTATATCA GGACAGCAAC	540

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ACGGAGCAAA ACTTTCAGCT TGCAAAG

27

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapien
 - (F) TISSUE TYPE: Carcinoma

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(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Membrane Specific Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Thr Glu Gln Asn Phe Gln Leu Ala Lys
1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCTTCGGCA TCCCCAGCTTG CAAACAAAAT TGTTCT

36

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGAACAAATT TGTTTGCAAG CTGGGATGCC AAGGAG

36

(2) INFORMATION FOR SEQ ID NO:34:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapien
 - (G) CELL TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapien
 - (G) CELL TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Asp Glu Leu Lys Ala Glu
1 5

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapien
(G) CELL TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Asn Glu Asp Gly Asn Glu
1 5

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapien
(G) CELL TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Lys Ser Pro Asp Glu Gly
1 5

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapien
(G) CELL TYPE: Carcinoma

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(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ala Gly Ala Leu Val Leu Ala Gly Gly Phe Phe Leu Leu Gly Phe Leu
1 5 10 15

Phe